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FIGURE 1

ATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGTAGTCAATCTCCTTTTGCGACATGGTGCAG	70
ACCCCAATGCTCGAGATAATTGGAATTATACTCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGT	140
TTGCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGAT C I V L L Q H G A E P T I R N T D G R T A L D	210
TTAGCAGATCCATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGA	280
GGAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTAAATGTCAACTGCCACGCAAGTGATGG RSGNEEKMMALLTPLNVNCHAS <u>DG</u>	350
CAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTACTGCAA R K S T P L H L A A G Y N R V K I V Q L L L Q	420
CATGGACGTGATGTCCATGCTAAAGATAAAGGTGATCTGGTACCATTACACAATGCCTGTTCTTATGGTC H G R D V H A K D K G D L V P L H N A C S Y G	490
ATTATGAAGTAACTGAACTTTTGGTCAAGCATGGTGGCTGTGTAAATGCAATGGACTTGTGGCAATTCAC H Y E V T E L L V K H G G C V N A M D L W Q F T	560
CCTCTTCATGAGGCAGCTTCTAAGAACAGGGTTGAAGTATGTTCTCTTCTCTTAAGTTATGGTGCAGAC PLHEAASKNRVEVCSLLLSYGAD	630
CCAACACTGCTCAATTGTAAGAATAAAAGTGCTATAGACTTGGCTCCCACACCACAGTTAAAAGAAAG	700
TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCGAATCAAAAA L A Y E F K G H S L L Q A A R E A D V T R I K K	770
ACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACATGAAACAGCATTGCATTGTGCTGCT H L S L E M V N F K H P Q <u>T H E T A L H C A A</u>	840
GCATCTCCATATCCCAAAAGAAAGCAAATATGTGAACTGTTGCTAAGAAAAGGAGCAAACATCAATGAAA ASPYPKRKQICELLRKGANINE	910
AGACTAAAGAATTCTTGACTCCTCTGCACGTGGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGT K T K E F L T P L H V A S E K A H N D V V E V V	980
GGTGAAACATGAAGCAAAGGTTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATAT V K H E A K V N A L D N L G Q T S L H R A A Y	1050
TGTGGTCATCTACAAACCTGCCGCCTACTCCTGAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGG C G H L Q T C R L L L S Y G C D P N $ m I$ I S L $ m Q$	1120
GCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTCATTAGGTAA G F T A L Q M G N E N V Q Q L L Q E G 1 S L G N	1190
TTCAGAGGCAGACAGACAATTGCTGGAAGCTGCAAAGGCTGGAGATGTCGAAACTGTAAAAAAACTGTGT SEADRQLLEAAKAGDVETVKKLC	1260
ACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGCGTCAGTCTACACCACTTCATTTTGCAGCTGGGT T V Q S V N C R D I E G R Q S T P L H F A A G	1330
ATAACAGAGTGTCCGTGGTGGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGYNR VS VVE YLLQHG A DVHA K DK G G	1400
CCTTGTACCTTTGCACAATGCATGTTCTTACGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGA L V P L H N A C S Y G H Y E V A E L L V K H G	1470
GCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATG A V V N V A D L W K F T P L H E A A A K G K Y	1546
AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTACAAAAAAAA	161

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GGATCTTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGATGCAGCTTTGCTAGATGCT DLVKDGDTDIQDLLRGDAALLDA	1680
GCCAAGAAGGGTTGTTTAGCCAGAGTGAAGAAGTTGTCTTCTCCTGATAATGTAAATTGCCGCGATACCC $oldsymbol{ ext{A}}$ K $oldsymbol{ ext{G}}$ C $oldsymbol{ ext{L}}$ A $oldsymbol{ ext{K}}$ K $oldsymbol{ ext{G}}$ C $oldsymbol{ ext{L}}$ A $oldsymbol{ ext{K}}$ K $oldsymbol{ ext{K}}$ C $oldsymbol{ ext{R}}$ D $oldsymbol{ ext{T}}$	1750
AAGGCAGACATTCAACACCTTTACATTTAGCAGCTGGTTATAATAATTTAGAAGTTGCAGAGTATTTGTT $Q \hspace{0.1cm} G \hspace{0.1cm} R \hspace{0.1cm} H \hspace{0.1cm} S \hspace{0.1cm} T \hspace{0.1cm} P \hspace{0.1cm} L \hspace{0.1cm} H \hspace{0.1cm} L \hspace{0.1cm} A \hspace{0.1cm} G \hspace{0.1cm} Y \hspace{0.1cm} N \hspace{0.1cm} N \hspace{0.1cm} L \hspace{0.1cm} E \hspace{0.1cm} V \hspace{0.1cm} A \hspace{0.1cm} E \hspace{0.1cm} Y \hspace{0.1cm} L 0$	1820
ACAACACGGAGCTGATGTGAATGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATGCAGCATCTTAC Q H G A D V N A Q D K G G L I P L H N A A S Y	1890
GGGCATGTAGATGTAGCAGCTCTACTAATAAAGTATAATGCATCTCTCAATGCCACGGACAAATGGGCTT G H V D V A A L L I K Y N A S L N A T D K W A	1960
TCACACCTTTGCACGAAGCAGCCCAAAAGGGACGAACACAGCTTTGTGCTTGCT	2030
TGACCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTCAGCAGATGATGTCAGCGCT DPTLKNQEGQTDLVSADDVSA	2100
CTTCTGACAGCCATGCCCCCATCTGCTCTGCCCTCTTGTTACAAGCCTCAAGTGCTCAATGGTGTGA LLTAAAMPPSALPSCYKPQVLNGV	2170
GAAGCCCAGGAGCCACTGCAGATGCTCTCTCTTCAGGTCCATCTAGCCCATCAAGCCTTTCTGCAGCCAGRSPGSPSSLSAAS	2240
CAGTCTTGACAACTTATCTGGGAGTTTTTCAGAACTGTCTTCAGTAGTTAGT	2310
GCTTCCAGTTTGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTG A S S L E K K E V P G V D F S I T Q F V R N L	2380
GACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTGAGATGGGGCA G L E H L M D I F E R E Q I T L D V L V E M G H	2450
CAAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACTAATTAAAGGAGTCGAGAGA K E L K E I G I N A Y G H R H K L I K G V E R	2520
CTTATCTCCGGACAACAAGGTCTTAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTCTTA L I S G Q Q G L N P Y L T L N T S G S G T I L	2590
TAGATCTGTCTCCTGATGATAAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAAGTACAGTTCGAGAGCA I D L S P D D K E F Q S V E E E M Q S T V R E H	2660
CAGAGATGGAGGTCATGCAGGTGGAATCTTCAACAGATACAATATTCTCAAGATTCAGAAGGTTTGTAACR DGGHAGGTTTGTAACR NR NR N I L K I Q K V C N	2730
AAGAAACTATGGGAAAGATACACTCACCGGAGAAAAGAAGTTTCTGAAGAAAACCACAACCATGCCAATG K K L W E R Y T H R R K E V S E E N H N H A N	2800
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	2870
GTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGCTGAAAACTCTTCCAAAAGCAATCAAT	2940
TATGGAATTGGAGGAGGTACTGGGTGTCCAGTTCACAAAGACAGATCTTGTTACATTTGCCACAGGCAGC Y G I G G T G C P V H K D R S C Y I C H R Q	3010
TGCTCTTTTGCCGGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAAATGGCACATTCTCC L L F C R V T L G K S F L Q F S A M K M A H S P	3080
TCCAGGTCATCACTCAGTCACTGGTAGGCCCAGTGTAAATGGCCCTAGCATTAGCTGAATATGTTATTTAC PGHHSVTGRPSVNGLALAEYVIY	3150
AGAGGAGAACAGGCTTATCCTGAGTATTTAATTACTTACCAGATTATGAGGCCTGAAGGTATGGTCGATG R G E Q A Y P E Y L I T Y Q I M R P E G M V D	3220
GATAAATAGTTATTTTAAGAAACTAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTGGCCTCTACGT	3290

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TTTACTCCTTTGCTGAAAAAAATCATCTTGCCCACAGGCCTGTGGCAAAAGGATAAAAATGTGAACGAA 3360

GTTTAACATTCTGACTTGATAAAGCTTTAATAATGTACAG

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CONSTRUCT	STRUCTURE
N	PRO
C	
N + C	PRO
FL	PRO SH2

В		
CONSTRUCT	MEAN RLU (LIQUID ASSAY) (X 10 ³)	COLOUR INTENSITY (FILTER ASSAY)
pAS2.1	4	•
N	109	++
C	3	-
N + C	194	++
FL	242	· +++